

RESULT 1  
 PCT-US02-40423-19  
 ; Sequence 19, Application PC/TUS0240423  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stratagene  
 ; TITLE OF INVENTION: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR  
 ; FILE REFERENCE: 25436/2158  
 ; CURRENT APPLICATION NUMBER: PCT/US02/40423  
 ; CURRENT FILING DATE: 2002-12-17  
 ; NUMBER OF SEQ ID NOS: 127  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 775  
 ; TYPE: PRT  
 ; ORGANISM: Pyrococcus furiosus  
 PCT-US02-40423-19

Query Match 100.0%; Score 4038; DB 1; Length 775;  
 Best Local Similarity 100.0%;  
 Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDS	KIEEVKKITGERHG	60
Db	1	MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDS	KIEEVKKITGERHG	60
Qy	61	KIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRY		120
Db	61	KIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRY		120
Qy	121	LIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIMISYADENEAKVITWKNI	LDLPY	180
Db	121	LIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIMISYADENEAKVITWKNI	LDLPY	180
Qy	181	VEVVSSEEREMIKRFLRIIREKDPDIIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGSEPK		240
Db	181	VEVVSSEEREMIKRFLRIIREKDPDIIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGSEPK		240
Qy	241	MQRIGDMTAVEVKGRHFDLYHVITRTINLPITYTLEAVYEAIFGKPKKEKVYADEIAKAW	E	300
Db	241	MQRIGDMTAVEVKGRHFDLYHVITRTINLPITYTLEAVYEAIFGKPKKEKVYADEIAKAW	E	300
Qy	301	SGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVQQLWDVRSSTGNLVEWFLLRK		360
Db	301	SGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVQQLWDVRSSTGNLVEWFLLRK		360
Qy	361	AYERNEVAPNKPSEEEYQRRLRSEYTGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVS		420
Db	361	AYERNEVAPNKPSEEEYQRRLRSEYTGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVS		420
Qy	421	PTDLNLGCKNYDIAPQVGHKFKCDIPGFIPLSLGHLLERQKIKTKMKETQDPIEKILL		480
Db	421	PTDLNLGCKNYDIAPQVGHKFKCDIPGFIPLSLGHLLERQKIKTKMKETQDPIEKILL		480
Qy	481	DYRQKAIKLLANSFYGGYGYAKARWYCKEASVTAWRGRKYIELVWKELEEKFGFKVLYI		540

Db	481 DYRQKAIKLLANSFYGYGYAKARWYCKEAEVTAWGRKYIELVWKELEEKFGFKVLYI	540
Qy	541 <u>DT</u> DGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDE	600
Db	541 DTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDE	600
Qy	601 EGKVITRGLLEIVRRDWEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEK	660
Db	601 EGKVITRGLLEIVRRDWEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEK	660
Qy	661 LAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPGMVIGYIVLRGDGPISNRILAE	720
Db	661 LAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPGMVIGYIVLRGDGPISNRILAE	720
Qy	721 YDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNKKS	775
Db	721 YDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNKKS	775